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RAW SEQUENCE LISTING   DATE: 11/13/2001
PATENT APPLICATION: US/09/919,891   TIME: 15:27:19

Input Set : A:\211714US0X.txt
Output Set: N:\CRF3\11132001\I919891.raw

```
 3 <110> APPLICANT: BATHE, BRIGITTE
 4         MOCKEL, BETTINA
 5         PFEFFERLE, WALTER
 6         HUTHMACHER, KLAUS              ENTERED
 7         RUCKERT, CHRISTIAN
 8         KALINOWSKI, JORN
 9         PUHLER, ALFRED
10         BINDER, MICHAEL
11         GREISSINGER, DIETER
12         THIERBACH, GEORG
14 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE METH GENE
16 <130> FILE REFERENCE: 211714US0X
18 <140> CURRENT APPLICATION NUMBER: 09/919,891
19 <141> CURRENT FILING DATE: 2001-08-02
21 <150> PRIOR APPLICATION NUMBER: DE 10038050.6
22 <151> PRIOR FILING DATE: 2000-08-02
24 <150> PRIOR APPLICATION NUMBER: DE 10109687.9
25 <151> PRIOR FILING DATE: 2001-02-28
27 <150> PRIOR APPLICATION NUMBER: US 60/294,251
28 <151> PRIOR FILING DATE: 2001-05-31
30 <160> NUMBER OF SEQ ID NOS: 4
32 <170> SOFTWARE: PatentIn version 3.1
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 4301
36 <212> TYPE: DNA
37 <213> ORGANISM: Corynebacterium glutamicum
39 <220> FEATURE:
40 <221> NAME/KEY: CDS
41 <222> LOCATION: (385)..(4047)
42 <223> OTHER INFORMATION:
45 <400> SEQUENCE: 1
46 taagggtttt ggaggcattg gccgcgaacc catcgctggt catcccgggt ttgcgcatgc      60
48 cacgttcgta ttcataacca atcgcgatgc cttgagccca ccagccactg acatcaaagt     120
50 tgtccacgat gtgctttgcg atgtgggtgt gagtccaaga ggtggctttt acgtcgtcaa     180
52 gcaatttttag ccactcttcc cacggctttc cggtgccgtt gaggatagct tcaggggaca    240
54 tgcctggtgt tgagccttgc ggagtggagt cagtcatgcg accgagacta gtggcgcttt    300
56 gcctgtgttg cttaggcggc gttgaaaatg aactacgaat gaaaagttcg ggaattgtct    360
58 aatccgtact aagctgtcta caca atg tct act tca gtt act tca cca gcc       411
59                           Met Ser Thr Ser Val Thr Ser Pro Ala
60                             1               5
62 cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg ttg gca aac cat      459
63 His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala Leu Ala Asn His
64 10             15                  20                  25
66 gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc caa ggc ttt gac      507
67 Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu Gln Gly Phe Asp
68             30                  35                  40
70 ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg tgt aat gag att      555
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71 Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly Cys Asn Glu Ile
72          45              50              55
74 ctc aac gac acc cgc cct gat gtg ttg agg cag att cac cgc gcc tac      603
75 Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile His Arg Ala Tyr
76          60              65              70
78 ttt gag gcg gga gct gac ttg gtt gag acc aat act ttt ggt tgc aac      651
79 Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr Phe Gly Cys Asn
80      75              80              85
82 ctg ccg aac ttg gcg gat tat gac atc gct gat cgt tgc cgt gag ctt      699
83 Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg Cys Arg Glu Leu
84 90              95              100             105
86 gcc tac aag ggc act gca gtg gct agg gaa gtg gct gat gag atg ggg      747
87 Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala Asp Glu Met Gly
88              110             115             120
90 ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt tcc ctg gga cct      795
91 Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly Ser Leu Gly Pro
92              125             130             135
94 gga acg aag ctt cca tcg ctg ggc cat gca ccg tat gca gat ttg cgt      843
95 Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr Ala Asp Leu Arg
96          140             145             150
98 ggg cac tac aag gaa gca gcg ctt ggc atc atc gac ggt ggt ggc gat      891
99 Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp Gly Gly Gly Asp
100     155             160             165
102 gcc ttt ttg att gag act gct cag gac ttg ctt cag gtc aag gct gcg     939
103 Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln Val Lys Ala Ala
104 170             175             180             185
106 gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat aca ttc ttg ccc     987
107 Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp Thr Phe Leu Pro
108             190             195             200
110 att att tgc cac gtc acc gta gag acc acc ggc acc atg ctc atg ggt    1035
111 Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr Met Leu Met Gly
112             205             210             215
114 tct gag atc ggt gcc gcg ttg aca gcg ctg cag cca ctg ggt atc gac    1083
115 Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro Leu Gly Ile Asp
116         220             225             230
118 atg att ggt ctg aac tgc gcc acc ggc cca gat gag atg agc gag cac    1131
119 Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu Met Ser Glu His
120         235             240             245
122 ctg cgt tac ctg tcc aag cac gcc gat att cct gtg tcg gtg atg cct    1179
123 Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val Ser Val Met Pro
124 250             255             260             265
126 aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca gaa tac cca ctt    1227
127 Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala Glu Tyr Pro Leu
128             270             275             280
130 gag gct gag gat ttg gcg cag gcg ctg gct gga ttc gtc tcc gaa tat    1275
131 Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe Val Ser Glu Tyr
132         285             290             295
134 ggc ctg tcc atg gtg ggt ggt tgt tgt ggc acc aca cct gag cac atc    1323
135 Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr Pro Glu His Ile
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136        300                 305                 310
138 cgt gcg gtc cgc gat gcg gtg gtt ggt gtt cca gag cag gaa acc tcc    1371
139 Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu Gln Glu Thr Ser
140     315                 320                 325
142 aca ctg acc aag atc cct gca ggc cct gtt gag cag gcc tcc cgc gag    1419
143 Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln Ala Ser Arg Glu
144 330                 335                 340                 345
146 gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc tcg gtg cca ttg    1467
147 Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr Ser Val Pro Leu
148                 350                 355                 360
150 tcc cag gaa acc ggc att tcc atg atc ggt gag cgc acc aac tcc aac    1515
151 Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg Thr Asn Ser Asn
152                 365                 370                 375
154 ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc gat tgg gaa aag    1563
155 Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly Asp Trp Glu Lys
156         380                 385                 390
158 tgt gtg gat att gcc aag cag caa acc cgc gat ggt gca cac atg ctg    1611
159 Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly Ala His Met Leu
160     395                 400                 405
162 gat ctt tgt gtg gat tac gtg gga cga gac ggc acc gcc gat atg gcg    1659
163 Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr Ala Asp Met Ala
164 410                 415                 420                 425
166 acc ttg gca gca ctt ctt gct acc agc tcc act ttg cca atc atg att    1707
167 Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu Pro Ile Met Ile
168                 430                 435                 440
170 gac tcc acc gag cca gag gtt att cgc aca ggc ctt gag cac ttg ggt    1755
171 Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu Glu His Leu Gly
172                 445                 450                 455
174 gga cga agc atc gtt aac tcc gtc aac ttt gaa gac ggc gat ggc cct    1803
175 Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp Gly Asp Gly Pro
176         460                 465                 470
178 gag tcc cgc tac cag cgc atc atg aaa ctg gta aag cag cac ggt gcg    1851
179 Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys Gln His Gly Ala
180     475                 480                 485
182 gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag gca cgt acc gct    1899
183 Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln Ala Arg Thr Ala
184 490                 495                 500                 505
186 gag cac aag gtg cgc att gct aaa cga ctg att gac gat atc acc ggc    1947
187 Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp Asp Ile Thr Gly
188         510                 515                 520
190 agc tac ggc ctg gat atc aaa gac atc gtt gtg gac tgc ctg acc ttc    1995
191 Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp Cys Leu Thr Phe
192         525                 530                 535
194 ccg atc tct act ggc cag gaa gaa acc agg cga gat ggc att gaa acc    2043
195 Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp Gly Ile Glu Thr
196         540                 545                 550
198 atc gaa gcc atc cgc gag ctg aag aag ctc tac cca gaa atc cac acc    2091
199 Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro Glu Ile His Thr
200     555                 560                 565
```

```
202 acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac cct gct gca cgc     2139
203 Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn Pro Ala Ala Arg
204 570                 575                 580                 585
206 cag gtt ctt aac tct gtg ttc ctc aat gag tgc att gag gct ggt ctg     2187
207 Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile Glu Ala Gly Leu
208                 590                 595                 600
210 gac tct gcg att gcg cac agc tcc aag att ttg ccg atg aac cgc att     2235
211 Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro Met Asn Arg Ile
212                 605                 610                 615
214 gat gat cgc cag cgc gaa gtg gcg ttg gat atg gtc tat gat cgc cgc     2283
215 Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val Tyr Asp Arg Arg
216         620                 625                 630
218 acc gag gat tac gat ccg ctg cag gaa ttc atg cag ctg ttt gag ggc     2331
219 Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln Leu Phe Glu Gly
220     635                 640                 645
222 gtt tct gct gcc gat gcc aag gat gct cgc gct gaa cag ctg gcc gct     2379
223 Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu Gln Leu Ala Ala
224 650                 655                 660                 665
226 atg cct ttg ttt gag cgt ttg gca cag cgc atc atc gac ggc gat aag     2427
227 Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile Asp Gly Asp Lys
228                 670                 675                 680
230 aat ggc ctt gag gat gat ctg gaa gca ggc atg aag gag aag tct cct     2475
231 Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys Glu Lys Ser Pro
232                 685                 690                 695
234 att gcg atc atc aac gag gac ctt ctc aac ggc atg aag acc gtg ggt     2523
235 Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met Lys Thr Val Gly
236             700                 705                 710
238 gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc gtg ctg caa tcg     2571
239 Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe Val Leu Gln Ser
240     715                 720                 725
242 gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa ccg ttc atg gaa     2619
243 Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu Pro Phe Met Glu
244 730                 735                 740                 745
246 gag gaa gca gaa gct acc gga tct gcg cag gca gag ggc aag ggc aaa     2667
247 Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu Gly Lys Gly Lys
248                 750                 755                 760
250 atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat atc ggc aag aac     2715
251 Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn
252                 765                 770                 775
254 ttg gtg gac atc att ttg tcc aac aac ggt tac gac gtg gtg aac ttg     2763
255 Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp Val Val Asn Leu
256             780                 785                 790
258 ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca gcg gaa gaa cac     2811
259 Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala Ala Glu Glu His
260     795                 800                 805
262 aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg aag tcc acc gtg     2859
263 Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val Lys Ser Thr Val
264 810                 815                 820                 825
266 gtg atg aag gaa aac ctt gag gag atg aac aac gcc ggc gca tcc aat     2907
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267 Val Met Lys Glu Asn Leu Glu Glu Met Asn Asn Ala Gly Ala Ser Asn
268             830                 835                 840
270 tac cca gtc att ttg ggt ggc gct gcg ctg acg cgt acc tac gtg gaa    2955
271 Tyr Pro Val Ile Leu Gly Gly Ala Ala Leu Thr Arg Thr Tyr Val Glu
272             845                 850                 855
274 aac gat ctc aac gag gtg tac acc ggt gag gtg tac tac gcc cgt gat    3003
275 Asn Asp Leu Asn Glu Val Tyr Thr Gly Glu Val Tyr Tyr Ala Arg Asp
276             860                 865                 870
278 gct ttc gag ggc ctg cgc ctg atg gat gag gtg atg gca gaa aag cgt    3051
279 Ala Phe Glu Gly Leu Arg Leu Met Asp Glu Val Met Ala Glu Lys Arg
280             875                 880                 885
282 ggt gaa gga ctt gat ccc aac tca cca gaa gct att gag cag gcg aag    3099
283 Gly Glu Gly Leu Asp Pro Asn Ser Pro Glu Ala Ile Glu Gln Ala Lys
284 890                 895                 900                 905
286 aag aag gcg gaa cgt aag gct cgt aat gag cgt tcc cgc aag att gcc    3147
287 Lys Lys Ala Glu Arg Lys Ala Arg Asn Glu Arg Ser Arg Lys Ile Ala
288             910                 915                 920
290 gcg gag cgt aaa gct aat gcg gct ccc gtg att gtt ccg gag cgt tct    3195
291 Ala Glu Arg Lys Ala Asn Ala Ala Pro Val Ile Val Pro Glu Arg Ser
292             925                 930                 935
294 gat gtc tcc acc gat act cca acc gcg gca cca ccg ttc tgg gga acc    3243
295 Asp Val Ser Thr Asp Thr Pro Thr Ala Ala Pro Pro Phe Trp Gly Thr
296             940                 945                 950
298 cgc att gtc aag ggt ctg ccc ttg gcg gag ttc ttg ggc aac ctt gat    3291
299 Arg Ile Val Lys Gly Leu Pro Leu Ala Glu Phe Leu Gly Asn Leu Asp
300     955                 960                 965
302 gag cgc gcc ttg ttc atg ggg cag tgg ggt ctg aaa tcc acc cgc ggc    3339
303 Glu Arg Ala Leu Phe Met Gly Gln Trp Gly Leu Lys Ser Thr Arg Gly
304 970                 975                 980                 985
306 aac gag ggt cca agc tat gag gat ttg gtg gaa act gaa ggc cga  cca    3387
307 Asn Glu Gly Pro Ser Tyr Glu Asp Leu Val Glu Thr Glu Gly Arg  Pro
308             990                 995                 1000
310 cgc ctg cgc tac  tgg ctg gat cgc ctg  aag tct gag ggc att  ttg     3432
311 Arg Leu Arg Tyr  Trp Leu Asp Arg Leu  Lys Ser Glu Gly Ile  Leu
312             1005                1010                1015
314 gac cac gtg gcc  ttg gtg tat ggc tac  ttc cca gcg gtc gcg  gaa     3477
315 Asp His Val Ala  Leu Val Tyr Gly Tyr  Phe Pro Ala Val Ala  Glu
316             1020                1025                1030
318 ggc gat gac gtg  gtg atc ttg gaa tcc  ccg gat cca cac gca  gcc     3522
319 Gly Asp Asp Val  Val Ile Leu Glu Ser  Pro Asp Pro His Ala  Ala
320             1035                1040                1045
322 gaa cgc atg cgc  ttt agc ttc cca cgc  cag cag cgc ggc agg  ttc     3567
323 Glu Arg Met Arg  Phe Ser Phe Pro Arg  Gln Gln Arg Gly Arg  Phe
324             1050                1055                1060
326 ttg tgc atc gcg  gat ttc att cgc cca  cgc gag caa gct gtc  aag     3612
327 Leu Cys Ile Ala  Asp Phe Ile Arg Pro  Arg Glu Gln Ala Val  Lys
328             1065                1070                1075
330 gac ggc caa gtg  gac gtc atg cca ttc  cag ctg gtc acc atg  ggt     3657
331 Asp Gly Gln Val  Asp Val Met Pro Phe  Gln Leu Val Thr Met  Gly
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VERIFICATION SUMMARY   DATE: 11/13/2001
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